

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/578,939
Source: IFWP
Date Processed by STIC: 05/19/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 05/19/2006

PATENT APPLICATION: US/10/578,939

TIME: 08:39:24

Input Set : F:\210850067SEQLIST.TXT

Output Set: N:\CRF4\05192006\J578939.raw

```

4 <110> APPLICANT: UAB Research Foundation
5     van Ginkel, Frederik W.
6     Briles, David E.
7     Watt, James M.
10 <120> TITLE OF INVENTION: COMPOSITION FOR REDUCING BACTERIAL
11     CARRIAGE AND CNS INVASION AND METHODS OF USING SAME
14 <130> FILE REFERENCE: 21085.0067P1
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/578,939
C--> 16 <141> CURRENT FILING DATE: 2006-05-09
16 <150> PRIOR APPLICATION NUMBER: 60/518,799
17 <151> PRIOR FILING DATE: 2003-11-10
19 <160> NUMBER OF SEQ ID NOS: 17
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 23
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
30     Synthetic Construct
32 <400> SEQUENCE: 1
33 atttctgtaa cagctaccaa cga                                23
35 <210> SEQ ID NO: 2
36 <211> LENGTH: 23
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial Sequence
40 <220> FEATURE:
41 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
42     Synthetic Construct
44 <400> SEQUENCE: 2
45 gaattccctg tcttttcaaa gtc                                23
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 20
49 <212> TYPE: DNA
50 <213> ORGANISM: Artificial Sequence
52 <220> FEATURE:
53 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
54     Synthetic Construct
56 <400> SEQUENCE: 3
57 ccgatacact ctcttcccga                                20
59 <210> SEQ ID NO: 4
60 <211> LENGTH: 20
61 <212> TYPE: DNA

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62 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
66     Synthetic Construct
68 <400> SEQUENCE: 4
69 acagttggtg ctaaggaggc                                20
71 <210> SEQ ID NO: 5
72 <211> LENGTH: 15
73 <212> TYPE: PRT
74 <213> ORGANISM: Artificial Sequence
76 <220> FEATURE:
77 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
78     Synthetic Construct
80 <400> SEQUENCE: 5
81 Val Trp Arg Leu Leu Ala Pro Pro Phe Ser Asn Arg Leu Leu Pro
82  1           5           10           15
84 <210> SEQ ID NO: 6
85 <211> LENGTH: 34
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
91     Synthetic Construct
93 <400> SEQUENCE: 6
94 cgcggtatcct catactgggt taggaaagtc gtcg                34
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 37
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
103     Synthetic Construct
105 <400> SEQUENCE: 7
106 ggaattccat atgccgacag cagaactacc taaaggc              37
108 <210> SEQ ID NO: 8
109 <211> LENGTH: 41
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
115     Synthetic Construct
117 <400> SEQUENCE: 8
118 ggaattccat atgctggcaa atgaaactca actttcgggg g         41
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 29
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =

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127      Synthetic Construct
129 <400> SEQUENCE: 9
130 cgcggatcca tcggtttga ccatcggag                29
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 38
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
139      Synthetic Construct
141 <400> SEQUENCE: 10
142 ggaattccat atgcgtattc cagcacttct caagacag        38
144 <210> SEQ ID NO: 11
145 <211> LENGTH: 21
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
151      Synthetic Construct
153 <400> SEQUENCE: 11
154 ggaacattac ctgcgaaaag g                        21
156 <210> SEQ ID NO: 12
157 <211> LENGTH: 19
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
163      Synthetic Construct
165 <400> SEQUENCE: 12
166 taccgcgagg cataacatc                        19
168 <210> SEQ ID NO: 13
169 <211> LENGTH: 5
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
175      Synthetic Construct
177 <400> SEQUENCE: 13
178 Leu Pro Glu Thr Gly
179 1          5
181 <210> SEQ ID NO: 14
182 <211> LENGTH: 5
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
188      Synthetic Construct
W--> 190 <221> NAME/KEY: VARIANT
191 <222> LOCATION: 3

```

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192 <223> OTHER INFORMATION: Xaa = any amino acid.

W--> 194 <400> 14

W--> 195 Leu Pro Xaa Thr Gly

196 1 5

198 <210> SEQ ID NO: 15

199 <211> LENGTH: 1035

200 <212> TYPE: PRT

201 <213> ORGANISM: S. pneumoniae

203 <400> SEQUENCE: 15

204 Met Ser Tyr Phe Arg Asn Arg Asp Ile Asp Ile Glu Arg Asn Ser Met

205 1 5 10 15

206 Asn Arg Ser Val Gln Glu Arg Lys Cys Arg Tyr Ser Ile Arg Lys Leu

207 20 25 30

208 Ser Val Gly Ala Val Ser Met Ile Val Gly Ala Val Val Phe Gly Thr

209 35 40 45

210 Ser Pro Val Leu Ala Gln Glu Gly Ala Ser Glu Gln Pro Leu Ala Asn

211 50 55 60

212 Glu Thr Gln Leu Ser Gly Glu Ser Ser Thr Leu Thr Asp Thr Glu Lys

213 65 70 75 80

214 Ser Gln Pro Ser Ser Glu Thr Glu Leu Ser Gly Asn Lys Gln Glu Gln

215 85 90 95

216 Glu Arg Lys Asp Lys Gln Glu Glu Lys Ile Pro Arg Asp Tyr Tyr Ala

217 100 105 110

218 Arg Asp Leu Glu Asn Val Glu Thr Val Ile Glu Lys Glu Asp Val Glu

219 115 120 125

220 Thr Asn Ala Ser Asn Gly Gln Arg Val Asp Leu Ser Ser Glu Leu Asp

221 130 135 140

222 Lys Leu Lys Lys Leu Glu Asn Ala Thr Val His Met Glu Phe Lys Pro

223 145 150 155 160

224 Asp Ala Lys Ala Pro Ala Phe Tyr Asn Leu Phe Ser Val Ser Ser Ala

225 165 170 175

226 Thr Lys Lys Asp Glu Tyr Phe Thr Met Ala Val Tyr Asn Asn Thr Ala

227 180 185 190

228 Thr Leu Glu Gly Arg Gly Ser Asp Gly Lys Gln Phe Tyr Asn Asn Tyr

229 195 200 205

230 Asn Asp Ala Pro Leu Lys Val Lys Pro Gly Gln Trp Asn Ser Val Thr

231 210 215 220

232 Phe Thr Val Glu Lys Pro Thr Ala Glu Leu Pro Lys Gly Arg Val Arg

233 225 230 235 240

234 Leu Tyr Val Asn Gly Val Leu Ser Arg Thr Ser Leu Arg Ser Gly Asn

235 245 250 255

236 Phe Ile Lys Asp Met Pro Asp Val Thr His Val Gln Ile Gly Ala Thr

237 260 265 270

238 Lys Arg Ala Asn Asn Thr Val Trp Gly Ser Asn Leu Gln Ile Arg Asn

239 275 280 285

240 Leu Thr Val Tyr Asn Arg Ala Leu Thr Pro Glu Glu Val Gln Lys Arg

241 290 295 300

242 Ser Gln Leu Phe Lys Arg Ser Asp Leu Glu Lys Lys Leu Pro Glu Gly

243 305 310 315 320

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```

244 Ala Ala Leu Thr Glu Lys Thr Asp Ile Phe Glu Ser Gly Arg Asn Gly
245          325          330          335
246 Lys Pro Asn Lys Asp Gly Ile Lys Ser Tyr Arg Ile Pro Ala Leu Leu
247          340          345          350
248 Lys Thr Asp Lys Gly Thr Leu Ile Ala Gly Ala Asp Glu Arg Arg Leu
249          355          360          365
250 His Ser Ser Asp Trp Gly Asp Ile Gly Met Val Ile Arg Arg Ser Glu
251          370          375          380
252 Asp Asn Gly Lys Thr Trp Gly Asp Arg Val Thr Ile Thr Asn Leu Arg
253 385          390          395          400
254 Asp Asn Pro Lys Ala Ser Asp Pro Ser Ile Gly Ser Pro Val Asn Ile
255          405          410          415
256 Asp Met Val Leu Val Gln Asp Pro Glu Thr Lys Arg Ile Phe Ser Ile
257          420          425          430
258 Tyr Asp Met Phe Pro Glu Gly Lys Gly Ile Phe Gly Met Ser Ser Gln
259          435          440          445
260 Lys Glu Glu Ala Tyr Lys Lys Ile Asp Gly Lys Thr Tyr Gln Ile Leu
261          450          455          460
262 Tyr Arg Glu Gly Glu Lys Gly Ala Tyr Thr Ile Arg Glu Asn Gly Thr
263 465          470          475          480
264 Val Tyr Thr Pro Asp Gly Lys Ala Thr Asp Tyr Arg Val Val Val Asp
265          485          490          495
266 Pro Val Lys Pro Ala Tyr Ser Asp Lys Gly Asp Leu Tyr Lys Gly Asn
267          500          505          510
268 Gln Leu Leu Gly Asn Ile Tyr Phe Thr Thr Asn Lys Thr Ser Pro Phe
269          515          520          525
270 Arg Ile Ala Lys Asp Ser Tyr Leu Trp Met Ser Tyr Ser Asp Asp Asp
271          530          535          540
272 Gly Lys Thr Trp Ser Ala Pro Gln Asp Ile Thr Pro Met Val Lys Ala
273 545          550          555          560
274 Asp Trp Met Lys Phe Leu Gly Val Gly Pro Gly Thr Gly Ile Val Leu
275          565          570          575
276 Arg Asn Gly Pro His Lys Gly Arg Ile Leu Ile Pro Val Tyr Thr Thr
277          580          585          590
278 Asn Asn Val Ser His Leu Asn Gly Ser Gln Ser Ser Arg Ile Ile Tyr
279          595          600          605
280 Ser Asp Asp His Gly Lys Thr Trp His Ala Gly Glu Ala Val Asn Asp
281          610          615          620
282 Asn Arg Gln Val Asp Gly Gln Lys Ile His Ser Ser Thr Met Asn Asn
283 625          630          635          640
284 Arg Arg Ala Gln Asn Thr Glu Ser Thr Val Val Gln Leu Asn Asn Gly
285          645          650          655
286 Asp Val Lys Leu Phe Met Arg Gly Leu Thr Gly Asp Leu Gln Val Ala
287          660          665          670
288 Thr Ser Lys Asp Gly Gly Val Thr Trp Glu Lys Asp Ile Lys Arg Tyr
289          675          680          685
290 Pro Gln Val Lys Asp Val Tyr Val Gln Met Ser Ala Ile His Thr Met
291          690          695          700
292 His Glu Gly Lys Glu Tyr Ile Ile Leu Ser Asn Ala Gly Gly Pro Lys

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 3

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:16; Line(s) 461

VERIFICATION SUMMARY

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L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:190 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:194 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0